

specification and substitute replacement pages 28-32 attached hereto as separate pages.

REMARKS

A copy of the corrected Sequence Listing in computer readable form is attached hereto. The content of the paper copy of the Sequence Listing and the copy of the Sequence Listing in computer readable form is the same, and includes no new matter.

It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11.0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

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## SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Seulberger, Harald  
Lerchl, Jenms  
Schmidt, Ralf-Michael  
Krupinska, Karin  
Falk, Jon

<120> DNA sequence encoding a hydroxyphenylpyruvate dioxygenase, and its overproduction in plants

<140> US 09/462,629  
<141> 2000-01-11

<150> PCT/EP98/03832  
<151> 1998-06-23

<160> 2

<170> WordPerfect version 6.1

<210> 1  
<211> 1565  
<212> DNA  
<213> hppd from barley

<220>  
<221> CDS  
<222> 9 ... 1313

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Met Pro Pro Thr Pro Thr Pro Ala Ala Thr Gly Ala Ala  
1 5 10 50

gcc gcg gtg acg ccg gag cac gcg cga ccg cac cga atg gtc cgc ttc  
Ala Ala Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe  
15 20 25 30 98

aac ccg cgc agc gac cgc ttc cac acg ctc tcc ttc cac cac gtc gag  
Asn Pro Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu  
35 40 45 146

ttc tgg tgc gcg gac gcc tcc gcc ggc cgc ttc gcg ttc gcg  
Phe Trp Cys Ala Asp Ala Ala Ser Ala Gly Arg Phe Ala Phe Ala  
50 55 60 194

ctc ggc gcg ccg ctc gcc agg tcc gac ctc tcc acg ggg aac tcc  
Leu Gly Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser  
65 70 75 242

gcg cac gcc tcc cag ctg ctc cgc tcg ggc tcc ctc gcc ttc ctc ttc  
290

Ala His Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe	80	85	90	
acc gcg ccc tac gcc aac ggc tgc gac gcc gcc acc gcc tcc ctg ccc				338
Thr Ala Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro				
95	100	105	110	
tcc ttc tcc gcc gac gcc gcg cgc cgg ttc tcc gcc gac cac ggg atc				386
Ser Phe Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile				
115	120	125		
gcg gtg cgc tcc gta gcg ctg cgc gtc gca gac gcc gac ggg gcc ttc				434
Ala Val Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe				
130	135	140		
cgc gcc agt cgt cga cgg ggc gcg cgc ccg gcc ttc gcc ccc gtg gac				482
Arg Ala Ser Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp				
145	150	155		
ctc ggc cgc ggc ttc gcg ttc gcg gag gtc gag ctc tac ggc gac gtc				530
Leu Gly Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val				
160	165	170		
gtg ctc cgc ttc gtc agc cac ccg gac ggc acg gac gtg ccc ttc ttg				578
Val Leu Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu				
175	180	185	190	
ccg ggg ttc gag ggc gta acc aac ccg gac gcc gtg gac tac ggc ctg				626
Pro Gly Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu				
195	200	205		
acg cgg ttc gac cac gtc gtc ggc aac gtc ccg gag ctt gcc ccc gcc				674
Thr Arg Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala				
210	215	220		
gca gcc tac atc gcc ggg ttc acg ggg ttc cac gag ttc gcc gag ttc				722
Ala Ala Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe				
225	230	235		
acg gcg gag gac gtg ggc acg acc gag agc ggg ctc aac tcg gtg gtg				770
Thr Ala Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val				
240	245	250		
ctc gcc aac aac tcg gag ggc gtg ctg ccg ctc aac gag ccg gtg				818
Leu Ala Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val				
255	260	265	270	
cac ggc acc aag cgc cgg agc cag ata cag acg ttc ctg gaa cac cac				866
His Gly Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His				
275	280	285		
ggc ggc ccg ggc gtg cag cac atc gcg gtg gcc agc agt gac gtg ctc				914
Gly Gly Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu				

290

295

300

agg acg ctc agg aag atg cgt gcg cgc tcc gcc atg ggc ggc ttc gac Arg Thr Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp 305	310	315	962	
ttc ctg cca ccc ccg ctg ccg aag tac tac gaa ggc gtg cga cgc ctt Phe Leu Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu 320	325	330	1010	
gcc ggg gat gtc ctc tcg gag gcg cag atc aag gaa tgc cag gag ctg Ala Gly Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu 335	340	345	1058	
ggt gtg ctc gtc gat agg gac gac caa ggg gtg ttg ctc caa atc ttc Gly Val Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe 355	360	365	1106	
acc aag cca gta ggg gac agg ccg acc ttg ttc ctg gag atg atc cag Thr Lys Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln 370	375	380	1154	
agg atc ggg tgc atg gag aag gac gag aga ggg gaa gag tac cag aag Arg Ile Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys 385	390	395	1202	
ggt ggc tgc ggc ggg ttc ggc aaa ggc aac ttc tcc gag ctg ttc aag Gly Gly Cys Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys 400	405	410	1250	
tcc att gaa gat tac gag aag tcc ctt gaa gcc aag caa tct gct gca Ser Ile Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala 415	420	425	430	1298
gtt cag gga tca taggatagaa gctggtcctt gtatcatgggt ctcatggagc Val Gln Gly Ser				1350
aaaagaaaaac aatgttgttt gtaatatgcg tcgcacaatt atatcaatgt tataattgggt				1410
gaagctgaag acagatgtat cctatgtatg atgggtgtaa tggatggtag aggggctcac				1470
acatgaagaa aatgttagcgt tgacattgtt gtacaatctt gcttgcaagt aaaataaaga				1530
acagattttg agttctgcaa aaaaaaaaaaaa aaaaa				1565

&lt;210&gt; 2

&lt;211&gt; 434

&lt;212&gt; PRT

&lt;213&gt; hppd from barley

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 1 5 10 15

Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe Asn Pro  
 20 25 30

Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu Phe Trp  
 35 40 45

Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly  
 50 55 60

Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Ala His  
 65 70 75 80

Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe Thr Ala  
 85 90 95

Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe  
 100 105 110

Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile Ala Val  
 115 120 125

Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala  
 130 135 140

Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp Leu Gly  
 145 150 155 160

Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu  
 165 170 175

Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu Pro Gly  
 180 185 190

Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu Thr Arg  
 195 200 205

Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala Ala Ala  
 210 215 220

Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe Thr Ala  
 225 230 235 240

Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val Leu Ala  
 245 250 255

Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val His Gly  
 260 265 270

Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His Gly Gly  
 275 280 285

Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu Arg Thr  
290 295 300

Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp Phe Leu  
305 310 315 320

Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu Ala Gly  
325 330 335

Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu Gly Val  
340 345 350

Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe Thr Lys  
355 360 365

Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln Arg Ile  
370 375 380

Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys Gly Gly  
385 390 395 400

Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys Ser Ile  
405 410 415

Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala Val Gln  
420 425 430

Gly Ser--.